

TTATTAGGTTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT  
 1 -----+-----+-----+-----+-----+-----+ 60  
 AATAATCCAAAAATGGATGGGTCCTTTTCGGTTGGTTGGAGCTAGAGAACATCTAGACAA  
 CTCTAAACGAACCTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC  
 61 -----+-----+-----+-----+-----+-----+ 120  
 GAGATTTGCTTGAAATTTTAGACACATCGACAGCGAGCCGACGTACGGATCACGTGGATG  
  
 ...  
  
 GTACTATGACAAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAG  
 15061 -----+-----+-----+-----+-----+-----+ 15120  
 CATGATACTGTTTATCTGTCAAAGTAGTCTTTAATAACTTCAGTTATCGGCGGTGATCTC  
 GAGCTACTGTGGTAATTGGAACAAGCAAGTTTTACGGTGGCTGGCATAATATGTTAAAAA  
 15121 -----+-----+-----+-----+-----+-----+ 15180  
 CTCGATGACACCATTAACCTTGTTCTGTTCAAATGCCACCGACCGTATTATACAATTTTT  
  
CANADA first PCR CA  
 CTGTTTACAGTGATGTAGAACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACA  
 15181 -----+-----+-----+-----+-----+-----+ 15240  
 GACAAATGTCACTACATCTTTGAGGTGTGGAATACCCAACCCTAATAGGTTTTACACTGT  
 GAGCCATGCCTAACATG  
 GAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGTTCTTGCTCGCAAACATAACA  
 15241 -----+-----+-----+-----+-----+-----+ 15300  
 CTCGGTACGGATTGTACGAATCCTATTACCGGAGAGACAAGAACGAGCGTTTGTATTGT  
 CTTGCTGTAACCTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAA  
 15301 -----+-----+-----+-----+-----+-----+ 15360  
 GAACGACATTGAATAGTGTGGCAAAGATGTCCAATCGATTGCTCACACGCGTTCATAATT  
  
CANADA second PCR TGTAAACCAGGTGGAAC  
 GTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTG  
 15361 -----+-----+-----+-----+-----+-----+ 15420  
 CACTCTACCAGTACACACCGCCGAGTGATATAACAATTTGGTCCACCTTGTAGTAGGCCAC  
 ATGCTACAACCTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATG  
 15421 -----+-----+-----+-----+-----+-----+ 15480  
 TACGATGTTGACGAATACGATTATCACAGAAATTGTAAACAGTTCGACAATGTCGGTTAC  
 TAAATGCACTTCTTTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTAC  
 15481 -----+-----+-----+-----+-----+-----+ 15540  
 ATTTACGTGAAGAAAGTTGACTACCATTATTCTATCGACTGTTTCATACAGGCGTTAGATG  
 GCGTTAGATG

**FIG. 1**

AACACAGGCTCTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG  
 15541 -----+-----+-----+-----+-----+-----+ 15600  
 TTGTCTCCGAGATACTCACAGAGATATCTTTATCCCTACAAGTACTTAAGCACCTAC  
 TTGTGTCC CANADA second PCR  
  
 AGTTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATTCTTTCTGATGATGCCGTTG  
 15601 -----+-----+-----+-----+-----+ 15660  
 TCAAAATGCGAATGGACGCATTTGTAAAGAGGTACTACTAAGAAAGACTACTACGGCAAC  
 GCGAATGGACGCATTTGTAA CANADA first PCR  
  
 TGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGCTAGCATTAAAGAACTTTAAGG  
 15661 -----+-----+-----+-----+-----+ 15720  
 ACACGATATTGTCATTGATACGCCGAGTTCCAAATCATCGATCGTAATTCTTGAAATTCC  
  
 CAGTTCTTTATTATCAAAATAATGTGTTTCATGTCTGAGGCAAAATGTTGGACTGAGACTG  
 15721 -----+-----+-----+-----+-----+ 15780  
 GTCAAGAAATAATAGTTTTATTACACAAGTACAGACTCCGTTTTACAACCTGACTCTGAC  
  
 ...  
  
 GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATA  
 18001 -----+-----+-----+-----+-----+ 18060  
 CATCATTCTAGTAATGACCAGAAGTAGGATGTGTCCGTGGATGTGTGGAGTCGCAACTAT  
  
 TAAAGTTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT  
 18061 -----+-----+-----+-----+-----+ 18120  
 ATTTCAAGTTCTGACTTCCTAATACACAAGTGTATGGTCCGTATGGTTTCCTGTACTGGA  
  
BNioutS2 ATGAATTACCAAGTCAATGGTTAC  
 ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTA  
 18121 -----+-----+-----+-----+-----+ 18180  
 TGGCATCTGAGTAGAGATACTACCCAAAGTTTTACTTAATGGTTCAGTTACCAATGGGAT  
  
BNlinS GAAGCTATTCGTCACGTTTCG  
 ATATGTTTATCACCCGCGAAGAAGCTATTCGTCACGTTTCGTGCGTGGATTGGCTTTGATG  
 18181 -----+-----+-----+-----+-----+ 18240  
 TATACAAATAGTGGGCGCTTCTTCGATAAGCAGTGCAAGCACGCACCTAACCGAAACTAC  
  
 TAGAGGGCTGTCATGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGAT  
 18241 -----+-----+-----+-----+-----+ 18300  
 ATCTCCCGACAGTACGTTGATCTCTACGACACCCATGATTGGATGGAGAGGTCGATCCTA  
 GAGGTGCGATCCTA  
  
 TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACA  
 18301 -----+-----+-----+-----+-----+ 18360  
 AAAGATGTCCACAATTGAATCATCGACATGGCTGACCAATACAAGTGTGACTTTTATTGT  
 AAAGATGTC BNlinAS  
 CATCGACATGGCTGACCAATAC BNioutAS

**FIG. 1 cont.**

CAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACATCTTATAC  
 18361 -----+-----+-----+-----+-----+-----+ 18420  
 GTCTTAAGTGGTCTCAATTACGTTTTGGAGGTGGTCCACTGGTCAAATTTGTAGAATATG

CACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCCTATTAAGATAGTACAAATGCTCA  
 18421 -----+-----+-----+-----+-----+-----+ 18480  
 GTGAGTACATATTTCCGAACGGGACCTTACATCACGCATAATTCTATCATGTTTACGAGT

...

TACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCC  
 28381 -----+-----+-----+-----+-----+-----+ 28440  
 ATGGCTTCTCGATGGGCTGCTCAAGCACCACCACTGCCGTTTTACTTTCTCGAGTCGGGG

AGATGGTACTTCTATTACCTAGGAAGTGGCCAGAAAGCTTCACTTCCCTACGGCGCTAAC  
 28441 -----+-----+-----+-----+-----+-----+ 28500  
 TCTACCATGAAGATAATGGATCCTTGACCGGTCTTCGAAGTGAAGGGATGCCGCGATTG

CIID-28506F AGGCATCGTATGGGTTGCA  
CIID-28529T AGGGAGCCTTGAATACACCCAAAGACCA  
 AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATT  
 28501 -----+-----+-----+-----+-----+-----+ 28560  
 TTTCTTCCGTAGCATACCCAACGTTGACTCCCTCGGAAGTTATGTGGGTTTCTGGTGTAA

GGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAAGTTCCCTCAAGGAACAACA  
 28561 -----+-----+-----+-----+-----+-----+ 28620  
 CCGTGGGCGTTAGGATTATTGTTACGACGGTGGCACGATGTTGAAGGAGTTCCTTGTGT  
 TTGTTGT

TTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCC  
 28621 -----+-----+-----+-----+-----+-----+ 28680  
 AACGGTTTTCCGAAGATGCGTCTCCCTTCGTCTCCGCCGTCAGTTCGGAGAAGAGCGAGG  
 AACGGTTTTCCGAAG CIID-28614R

TCATCACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCT  
 28681 -----+-----+-----+-----+-----+-----+ 28740  
 AGTAGTGCATCAGCGCCATTAAGTTCTTTAAGTTGAGGACCGTCGTCATCCCCTTTAAGA

CCTGCTCGAATGGCTAGCGGAGGTGGTGAACTGCCCTCGCGCTATTGCTGCTAGACAGA  
 28741 -----+-----+-----+-----+-----+-----+ 28800  
 GGACGAGCTTACCGATCGCCTCCACCACTTTGACGGGAGCGCGATAACGACGATCTGTCT

TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAAGGCCAAACTGTC  
 28801 -----+-----+-----+-----+-----+-----+ 28860  
 AACTTGTCGAACTCTCGTTTCAAAGACCATTTCGGTTGTTGTTGTTCCGGTTTGACAG

CIID-28891F AAGCCTCGCCAAAAACGTAC  
 ACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAA  
 28861 -----+-----+-----+-----+-----+-----+ 28920  
 TGATTCTTTAGACGACGACTCCGTAGATTTTTTCGGAGCGGTTTTTGCATGACGGTGTTTT

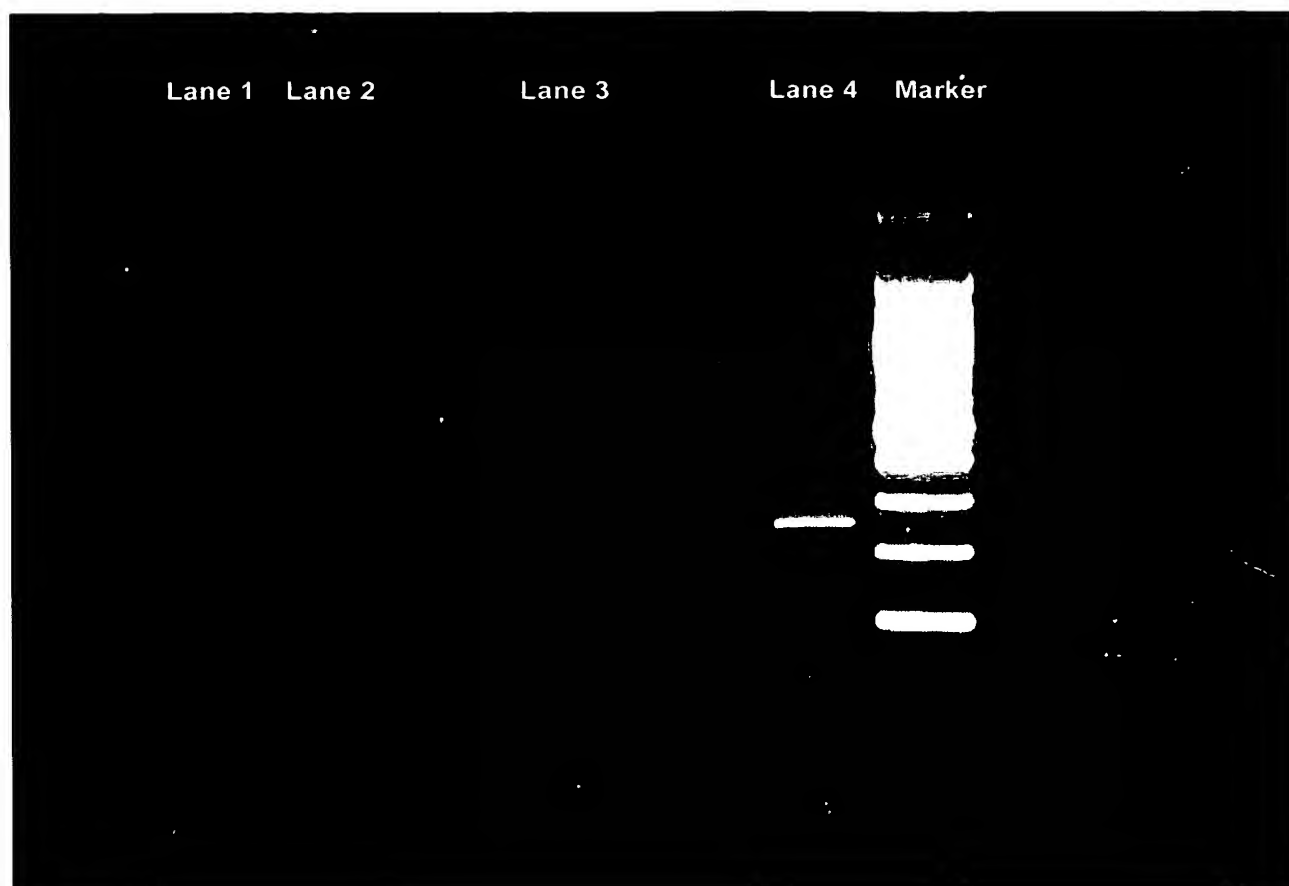
**FIG. 1 cont.**

CAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTC  
 28921 -----+-----+-----+-----+-----+ 28980  
 GTCATGTTGCAGTGAGTTCGTAAACCCTCTGCACCAGGTCTTGTTTGGGTTCCCTTTAAAG  
  
 GGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAA  
 28981 -----+-----+-----+-----+-----+ 29040  
 CCCCTGGTTCTGGATTAGTCTGTTCCCTTGACTAATGTTTGTAAACCGGCGTTTAACGTGTT  
  
CIID-29074T TCACGCATTGGCATGGAAGTCACAC  
 TTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT  
 29041 -----+-----+-----+-----+-----+ 29100  
 AAACGAGGTTACGGAGACGTAAGAAACCTTACAGTGCGTAACCGTACCTTCAGTGTGGA  
 A  
  
 TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTC  
 29101 -----+-----+-----+-----+-----+ 29160  
 AGCCCTTGTAACCGACTGAATAGTACCTCGGTAATTTAACCTACTGTTTCTAGGTGTAAAG  
 AGCCCTTGTAACCGACTGAA CIID-29100R  
  
 AAAGACAACGTCACTACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACA  
 29161 -----+-----+-----+-----+-----+ 29220  
 TTTCTGTTGCAGTATGACGACTTGTTCTGTGTAAGTGCATGTTTTGTAAAGGGTGGTTGT  
  
 GAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAA  
 29221 -----+-----+-----+-----+-----+ 29280  
 CTCGGATTTTTCTGTTTTCTTTTTCTGACTACTTCGAGTCGGAAACGGCGTCTCTGTT  
  
 AAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAA  
 29281 -----+-----+-----+-----+-----+ 29340  
 TTCTTCGTGCGGTGACACTGAGAAGAAGGACGCCGACTGTACCTACTAAAGAGGTCTGTT  
  
CIID-29398F ATG  
 CTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAAACACTCATGATG  
 29341 -----+-----+-----+-----+-----+ 29400  
 GAAGTTTTTAAGGTACTCACCTCGAAGACGACTAAGTTGAGTCCGTATTTGTGAGTACTAC  
  
CIID-29426F AAACGTTTTTCGCAATTCCGT  
CIID-29405F CACAAGGCAGATGGGCTATGT  
 ACCACACAAGGCACATGG  
 ACCACACAAGGCAGATGGGCTATGTAAACGTTTTTCGCAATTCCGTTTACGATACATAGTC  
 29401 -----+-----+-----+-----+-----+ 29460  
 TGGTGTGTTCCGTCTACCCGATACATTTGCAAAAGCGTTAAGGCAAATGCTATGTATCAG  
  
 TACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAAGTAGGTTTAGTTAACTTTA  
 29461 -----+-----+-----+-----+-----+ 29520  
 ATGAGAACACGTCTTACTTAAGAGCATTGATTTGTCGTGTTTCATCCAAATCAATTGAAAT  
  
 ATCTCACATAGCAATCTTTAATCAATGTGTAAACATTAGGGAGGACTTGAAAGAGCCACCA  
 29521 -----+-----+-----+-----+-----+ 29580  
 TAGAGTGTATCGTTAGAAATTAGTTACACATTGTAATCCCTCCTGAACTTTCTCGGTGGT

**FIG. 1 cont.**

CIID-29584T TTTCATCGAGGCCACGCGGAGTAC  
 CATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAG  
 29581 -----+-----+-----+-----+-----+ 29640  
 GTAAAAGTAGCTCCGGTGCGCCTCATGCTAGCTCCCATGTCACTTATTACGATCCCTCTC  
 TGTCACTTATTGCGATCCCTCTC  
 GTCACTTATTGCGATCCCTCTC  
 TGTCACTTATTACGATCCCTCTC  
 CTTATTACGATCCCTCTC  
 TCCGGTGCGCCTCATGCTAGCT CIID-29592T  
  
 CTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG  
 29641 -----+-----+-----+-----+-----+ 29700  
 GACGGATATACCTTCTCGGGATTACACATTTTAATTAAAATCATCACGATAGGGGTACAC  
 G 29618R  
 G 29619R  
 G 29618-2R  
 GACGG CIID-29623R  
  
 ATTTTAATAGCTTCTTAGGAGAATGAC  
 29701 -----+-----+----- 29727  
 TAAAATTATCGAAGAATCCTCTTACTG

**FIG. 1 cont.**



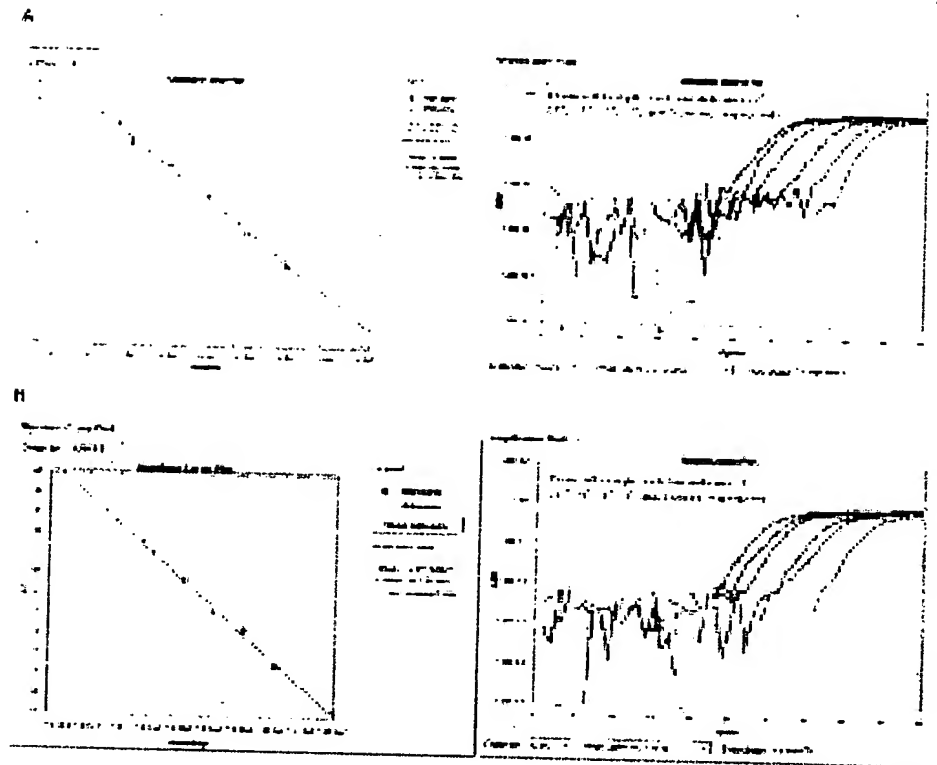
**FIG. 2**

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AGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCACCCGCA  
ATCCTAATAACAATGCTGCCACCGTGCTACAACCTCCTCAAGGAACAACATTGCCAAAAGGCTTCT  
ACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTAAT  
TCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAATGGCTAGCGGAGGTGG  
TGAAACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAAAGTTTCTGGTAA  
AGGCCAACAACAACAAGGCCAAACTGTCTACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTC  
GCCAAAAACGTA CTGCCACAAAACAGTACAACGTCCTCAAGCATTTGGGAGACGTGGTCCAGAA  
CAAACCCAAGGAAATTTCTGGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCC  
GCAAATTGCACAATTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGT  
CACACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATT  
CAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGAGC  
CTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAAAAAGCA  
GCCCACTGTGACTCTTCTTCTGCGGCTGACATGGATGATTTCTCCAGACAACCTTCAAAATTCATG  
AGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAAGGCAGATGGGC  
TATGTAAACGTTTTCTGCAATTCCGTTTACGATACATAGTCTACTCTTGTGCAGAATGAATTCTCGTA  
ACTAAACAGCACAAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAATGTGTAAC  
ATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTA  
CAGTGAATAATGCTAGGGAGAGC

**FIG. 3**

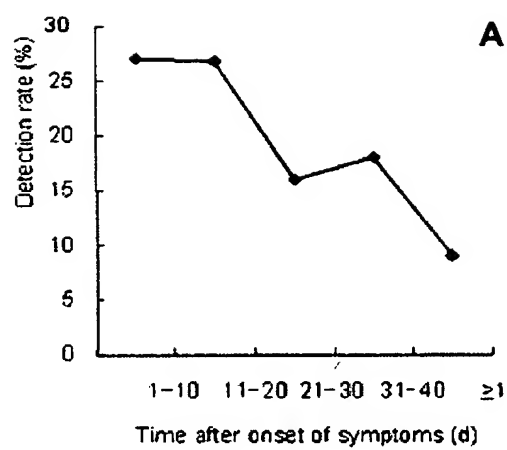
FIG. 4



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**FIG. 5A**



**FIG. 5B**

